

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 17:45:01 ; Search time 706.552 Seconds
(without alignments)
11734.281 Million cell updates/sec

Title: US-08-939-905D-1
Perfect score: 1244
Sequence: 1 atgggttcacatgcgtctatt.....ttaaggtaacttaataatca 1244

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

- Database : N_Geneseq_21:*
- 1: Geneseqn1980s:*
 - 2: Geneseqn1990s:*
 - 3: Geneseqn2000s:*
 - 4: Geneseqn2001as:*
 - 5: Geneseqn2001bs:*
 - 6: Geneseqn2002as:*
 - 7: Geneseqn2002bs:*
 - 8: Geneseqn2003as:*
 - 9: Geneseqn2003bs:*
 - 10: Geneseqn2003cs:*
 - 11: Geneseqn2003ds:*
 - 12: Geneseqn2004as:*
 - 13: Geneseqn2004bs:*
 - 14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1244	100.0	1244	2	AAV30460	Aav30460 Soybean s
2	1244	100.0	1244	2	AAV59077	Aav59077 Soybean s
3	1244	100.0	1244	14	ABB48290	Aeb48290 Soybean s
4	1244	100.0	1348	13	ADT18491	Adt18491 Plant CDN
5	1200	96.5	1200	14	ABB48312	Aeb48312 Soybean s
6	1056	84.9	1056	9	ADA01016	Ada01016 cDNA enco
7	920	74.0	1031	14	ABB48299	Aeb48299 Soybean s
8	669	53.8	3359	2	AAV59078	Aav59078 Soybean s
9	669	53.8	3359	14	ABB48311	Aeb48311 Soybean s
10	669	53.8	4700	2	AAV30461	Aav30461 Soybean s
11	669	53.8	4700	2	AAZ29902	Aaz29902 Nucleotid
12	669	53.8	4700	14	ABB48291	Aeb48291 Soybean s
13	624	50.2	4655	9	ADA01015	Ada01015 Genomic D
14	613	49.3	4648	9	ADA01019	Ada01019 Soybean D
15	562	45.2	1200	14	ABB48303	Aeb48303 Medicago
16	534.4	43.0	1200	14	ABB48300	Aeb48300 Medicago
17	532.4	42.8	1200	14	ABB48301	Aeb48301 Medicago
18	511.2	41.1	1200	14	ABB48302	Aeb48302 Medicago
19	363.2	29.2	1294	3	AAC33558	Aac33558 Arabidops

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OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 17:48:45 ; Search time 6171.24 Seconds
(without alignments)
11458.523 Million cell updates/sec

Title: US-08-939-905D-1
Perfect score: 1244
Sequence: 1 atgggtccatgcgtctatt.....ttaagggtacttaattaatca 1244

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_in.*
- 3: gb_env.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_ets.*
- 11: gb_sy.*
- 12: gb_un.*
- 13: gb_vi.*
- 14: gb_htg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1244	100.0	1244	15	SOYCVH63A	L78163 Glycine max
2	1056	84.9	1056	6	AR351556	AR351556 Sequence
3	920	74.0	1031	15	GMU41657	U41657 Glycine max
4	669	53.8	3359	15	SOYCVH63SC	L81148 Glycine max
5	669	53.8	4700	6	BD244520	BD244520 Seed coat
6	669	53.8	4700	15	AF014502	AF014502 Glycine m
7	624	50.2	4655	6	AR351555	AR351555 Sequence
8	616.4	49.5	1176	15	AF149277	AF149277 Phaseolus
9	613	49.3	4648	6	AR351558	AR351558 Sequence
10	569.2	45.8	1287	15	AF007211	AF007211 Glycine m
11	562	45.2	1220	15	MSRNAPE1A	X90692 M.sativa mR
12	559.4	45.0	1351	15	AF403735	AF403735 Lupinus a
13	552.4	44.4	1199	15	AB193818	AB193818 Pisum sat
14	536.6	43.1	1311	15	SSNPEROXIB	L36111 Stylosanthe
15	534.4	43.0	1238	15	MSRNAPE1B	X90693 M.sativa mR
16	532.4	42.8	1287	15	MSRNAPE1C	X90694 M.sativa mR
17	529.4	42.6	1246	15	AB193817	AB193817 Pisum sat
18	526.4	42.3	1462	15	AB193820	AB193820 Pisum sat

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OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 17:48:45 ; Search time 23315.8 Seconds
(without alignments)
11458.523 Million cell updates/sec

Title: US-08-939-905D-2
Perfect score: 4700
Sequence: 1 tagataaaaaaatgggatat.....ttaagggtacttaattaatca 4700

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4700	100.0	4700	6	BD244520 Seed coat
2	4700	100.0	4700	15	AF014502 Glycine m
3	4632.6	98.6	4655	6	AR351555 Sequence
4	4613.6	98.2	4648	6	AR351558 Sequence
5	3359	71.5	3359	15	SOYCVH63SC
6	669	14.2	1244	15	SOYCVH63A
7	559	11.9	1031	15	GMU41657
8	481	10.2	1056	6	AR351556 Sequence
9	295.6	6.3	4441	15	MSA306689
10	286.4	6.1	1176	15	AF149277
11	264.2	5.6	1220	15	MSRNAPE1A
12	255.4	5.4	1351	15	AF403735
13	249.8	5.3	1311	15	SSNPEROX1B
14	248.2	5.3	1199	15	AB193818
15	240.4	5.1	2428	15	POPP2
16	238.4	5.1	1271	15	ALFPXDA
17	237.2	5.0	1287	15	MSRNAPE1C
18	235.4	5.0	1170	15	AB087838

19	235.4	5.0	1462	15	AB193820	AB193820 Pisum sat
20	232.8	5.0	1224	15	AB193819	AB193819 Pisum sat
21	232.8	5.0	1287	15	AF007211	AF007211 Glycine m
22	229	4.9	1238	15	MSRNAPE1B	X90693 M.sativa mR
23	223.4	4.8	1246	15	AB193817	AB193817 Pisum sat
24	220.4	4.7	1019	15	AF405327	AF405327 Lupinus a
25	218.4	4.6	1169	15	ALFPXDC	L36157 Medicago sa
26	187	4.0	1371	15	PTXP4PER	X97351 P.trichocar
27	180	3.8	71277	15	AP002032	AP002032 Arabidops
28	179.6	3.8	1279	15	IBA242742	AJ242742 Ipomoea b
29	179	3.8	3040	15	POPP1	D38050 Populus kit
30	178.8	3.8	1170	15	POPPB	D30653 Populus kit
31	176.2	3.7	1291	15	AY519359	AY519359 Arabidops
32	174.8	3.7	96953	15	AC149540	AC149540 Populus t
33	173	3.7	1212	15	ATPATPA2A	X99952 A.thaliana
34	173	3.7	1233	15	AY056186	AY056186 Arabidops
35	173	3.7	1294	15	AY087674	AY087674 Arabidops
36	172.2	3.7	1143	15	POPP01	D83224 Populus nig
37	171.6	3.7	1836	15	POPP02	D83225 Populus nig
38	170.2	3.6	1039	15	AY096713	AY096713 Arabidops
39	169.2	3.6	1008	6	AX507019	AX507019 Sequence
40	169.2	3.6	1008	6	AX651264	AX651264 Sequence
41	168.8	3.6	1267	15	AF479623	AF479623 Ficus car
42	167.8	3.6	1324	15	AF488305	AF488305 Gossypium
43	167.6	3.6	1414	15	AY519360	AY519360 Arabidops
44	165.8	3.5	959	15	AB206042	AB206042 Populus a
45	164.2	3.5	1461	15	PTXP1PER	X97348 P.trichocar
46	162.6	3.5	1202	15	PTXP2PER	X97349 P.trichocar
47	162.6	3.5	1222	15	PTXP3PER	X97350 P.trichocar
48	160.2	3.4	1077	6	AX507285	AX507285 Sequence
49	160.2	3.4	1077	6	AX651273	AX651273 Sequence
50	160.2	3.4	1108	15	BT008584	BT008584 Arabidops
51	160.2	3.4	1296	15	AK118827	AK118827 Arabidops
52	160.2	3.4	1351	15	AY088509	AY088509 Arabidops
53	160	3.4	2733	15	HRAPRXC3	D90116 Armoracia r
54	158.6	3.4	1115	15	POPPA	D30652 Populus kit
55	156.8	3.3	8056	6	AX599046	AX599046 Sequence
56	156.4	3.3	2459	15	AF149280	AF149280 Phaseolus
57	155.8	3.3	84504	14	AP007910	AP007910 Lotus cor
58	155.6	3.3	1390	15	AY206410	AY206410 Ipomoea b
59	153.4	3.3	81467	15	AC004683	AC004683 Arabidops
60	151.8	3.2	3020	15	ATHPRECA	M58381 Arabidopsis
61	151.6	3.2	1268	15	LINPEROX	L07554 Linum usita
62	151.4	3.2	954	15	POPHPOX14	D13683 Populus kit
63	150.2	3.2	1050	6	AX589923	AX589923 Sequence
64	150.2	3.2	1120	15	BT001238	BT001238 Arabidops
65	150.2	3.2	1199	15	AF452385	AF452385 Arabidops
66	150.2	3.2	1221	15	AY099555	AY099555 Arabidops
67	148.6	3.2	1050	6	CQ804770	CQ804770 Sequence
68	148.6	3.2	1050	6	AX412629	AX412629 Sequence
69	148.6	3.2	1050	6	AX412630	AX412630 Sequence
70	148.6	3.2	1050	6	AX589921	AX589921 Sequence
71	148.6	3.2	1050	6	AX651689	AX651689 Sequence
72	148.6	3.2	1081	15	AY059106	AY059106 Arabidops
73	148.6	3.2	1177	15	AF452388	AF452388 Arabidops
74	148.6	3.2	1248	15	AY035033	AY035033 Arabidops
75	148.2	3.2	155108	14	AP007528	AP007528 Lotus cor
76	145.2	3.1	3289	15	HRAHRPCB	M37157 A.rusticana
77	143.4	3.1	3261	15	TOBPXD	D11396 Nicotiana t
78	142.2	3.0	753	15	ATP29A	Y11794 A.thaliana
79	141.8	3.0	1366	15	AJ781007	AJ781007 Raphanus
80	140	3.0	3436	15	ATHPRXCA	M58380 Arabidopsis
81	140	3.0	85109	15	ATT2J13	AL132967 Arabidops
82	140	3.0	129757	15	ATP2K15	AL132956 Arabidops
83	138.2	2.9	975	6	AX081286	AX081286 Sequence
84	138.2	2.9	987	15	AF455807	AF455807 Nicotiana
85	138.2	2.9	1196	15	LECEV11A	X71593 L.esculentu
86	137.8	2.9	766	15	AY423440	AY423440 Brassica
87	137.2	2.9	3944	15	LEY19023	Y19023 Lycopersico
88	136	2.9	762	15	AY521529	AY521529 Brassica
89	135.8	2.9	8056	6	AX599046	AX599046 Sequence
90	135.6	2.9	1064	6	AR034941	AR034941 Sequence
91	135.6	2.9	1064	6	I36771	I36771 Sequence 15

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OM nucleic - nucleic search, using sw model
Run on: April 11, 2006, 17:45:01 ; Search time 2669.45 Seconds
(without alignments)
11734.281 Million cell updates/sec

Title: US-08-939-905D-2
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Maximum Match 100%
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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4700	100.0	4700	2 AAV30461	Aav30461 Soybean s
2	4700	100.0	4700	2 AAZ29902	Aaz29902 Nucleotid
3	4700	100.0	4700	14 AEB48291	Aeb48291 Soybean s
4	4632.6	98.6	4655	9 ADA01015	Ada01015 Genomic D
5	4613.6	98.2	4648	9 ADA01019	Ada01019 Soybean D
6	3359	71.5	3359	14 AEB48311	Aeb48311 Soybean s
7	3355.8	71.4	3359	2 AAV59078	Aav59078 Soybean s
8	1532	32.6	1532	14 AEB48317	Aeb48317 Soybean s
9	1524	32.4	1524	14 AEB48318	Aeb48318 Soybean s
10	1074	22.9	1074	14 AEB48319	Aeb48319 Soybean s
11	669	14.2	1244	2 AAV30460	Aav30460 Soybean s
12	669	14.2	1244	2 AAV59077	Aav59077 Soybean s
13	669	14.2	1244	14 AEB48290	Aeb48290 Soybean s
14	669	14.2	1348	13 ADT18491	Adt18491 Plant CDN
15	625	13.3	1200	14 AEB48312	Aeb48312 Soybean s
16	559	11.9	1031	14 AEB48299	Aeb48299 Soybean s
17	481	10.2	1056	9 ADA01016	Ada01016 cDNA enco
18	467	9.9	467	14 AEB48320	Aeb48320 Soybean s
19	264.2	5.6	1200	14 AEB48303	Aeb48303 Medicago

20	238.4	5.1	1200	14	AEB48302	Aeb48302 Medicago
21	237.2	5.0	1200	14	AEB48301	Aeb48301 Medicago
22	229	4.9	1200	14	AEB48300	Aeb48300 Medicago
23	207	4.4	207	14	AEB48321	Aeb48321 Soybean s
24	173	3.7	1294	3	AAC33558	Aac33558 Arabidops
25	169.2	3.6	1008	6	ABZ113909	Abz113909 Arabidops
26	169.2	3.6	1008	8	ADA67811	Ada67811 Arabidops
27	160.2	3.4	1077	6	ABZ14175	Abz14175 Arabidops
28	160.2	3.4	1077	8	ADA67820	Ada67820 Arabidops
29	160.2	3.4	1351	3	AAC47823	Aac47823 Arabidops
30	156.8	3.3	8056	8	ABZ10246	Abz10246 Haematopo
31	153.2	3.3	691	10	ADK53798	Adk53798 Plant DNA
32	150.2	3.2	1050	8	ABZ42069	Abz42069 Arabidops
33	150.2	3.2	1095	3	AAC44309	Aac44309 Arabidops
34	148.6	3.2	787	6	ABN99084	Abn99084 Arabidops
35	148.6	3.2	1050	6	ADG87952	Adg87952 A. thalia
36	148.6	3.2	1050	6	ADG87951	Adg87951 A. thalia
37	148.6	3.2	1050	8	ABZ42068	Abz42068 Arabidops
38	148.6	3.2	1050	8	ADA68566	Ada68566 Arabidops
39	148.6	3.2	1050	12	ADN73286	Adn73286 Thale cre
40	148.6	3.2	1109	3	AAC42357	Aac42357 Arabidops
41	148.6	3.2	1194	3	AAC33091	Aac33091 Arabidops
42	147	3.1	1519	3	AAC52185	Aac52185 Arabidops
43	136.6	2.9	975	4	AAF62771	Aaf62771 Nicotiana
44	135.8	2.9	8056	8	ABZ10246	Abz10246 Haematopo
45	135.6	2.9	1064	2	AAQ87093	Aaq87093 Tpa-1 pha
46	135.6	2.9	1064	2	AAT63677	Aat63677 Peroxidas
47	135.6	2.9	1064	2	AAX03962	Aax03962 Anionic t
48	135.6	2.9	1270	2	AAQ87101	Aaq87101 The Tpa g
49	135.6	2.9	1270	2	AAT63685	Aat63685 Full-leng
50	135.6	2.9	1270	2	AAX03970	Aax03970 Full leng
51	127.6	2.7	1062	6	ABZ13652	Abz13652 Arabidops
52	127.6	2.7	1062	6	ADG87654	Adg87654 A. thalia
53	127.6	2.7	1062	6	ADG87655	Adg87655 A. thalia
54	127.6	2.7	1062	8	ADA68053	Ada68053 Arabidops
55	127.6	2.7	1062	13	ADU20634	Adu20634 A. thalia
56	127.6	2.7	1305	3	AACS1562	Aacs1562 Arabidops
57	127.6	2.7	2118	3	AAC51464	Aac51464 Arabidops
58	127.4	2.7	743	6	ABQ65469	Abq65469 Arabidops
59	127.4	2.7	1059	6	ABZ14520	Abz14520 Arabidops
60	127.4	2.7	1059	6	ADG87949	Adg87949 A. thalia
61	127.4	2.7	1059	8	ABZ42086	Abz42086 Arabidops
62	127.4	2.7	1177	3	AAC47869	Aac47869 Arabidops
63	125	2.7	975	4	AAF62773	Aaf62773 Synthetic
64	124.4	2.6	1065	3	AAC51563	Aac51563 Arabidops
65	124.4	2.6	1065	13	ADU20632	Adu20632 A. thalia
66	124.4	2.6	1065	13	ADU20411	Adu20411 A. thalia
67	124	2.6	1062	6	ABL59170	Ab159170 Nucleotid
68	124	2.6	1062	9	ACA63364	Aca63364 Gene enco
69	122.8	2.6	924	1	AAN81508	Aan81508 Horseradi
70	121.2	2.6	1065	3	AAC41661	Aac41661 Arabidops
71	121.2	2.6	1131	2	AAQ06207	Aaq06207 Cucumber
72	121.2	2.6	1305	3	AAC47953	Aac47953 Arabidops
73	120.8	2.6	1131	2	AAV62837	Aav62837 Cucumber
74	120.8	2.6	1131	2	AAV81611	Aav81611 Basic cuc
75	118	2.5	927	3	AAZ50790	Aaz50790 Horseradi
76	118	2.5	927	3	AAZ34931	Aaz34931 Horseradi
77	118	2.5	927	5	AAI65875	Aai65875 Nucleotid
78	118	2.5	927	6	ABL60811	Ab160811 Recombina
79	117.6	2.5	1055	1	AAN90762	Aan90762 Synthetic
80	117	2.5	975	4	AAF62772	Aaf62772 Synthetic
81	116.8	2.5	474	1	AAN94368	Aan94368 3' end ha
82	116.8	2.5	955	1	AAN90760	Aan90760 Synthetic
83	116.4	2.5	927	3	AAZ50793	Aaz50793 Horseradi
84	116.4	2.5	927	3	AAZ50794	Aaz50794 Horseradi
85	116.4	2.5	927	3	AAZ50798	Aaz50798 Horseradi
86	116.4	2.5	927	3	AAZ50791	Aaz50791 Horseradi
87	116.4	2.5	927	3	AAZ50792	Aaz50792 Horseradi
88	116.4	2.5	927	5	AAI65879	Aai65879 Nucleotid
89	116.4	2.5	927	5	AAI65878	Aai65878 Nucleotid
90	116.4	2.5	927	5	AAI65876	Aai65876 Nucleotid
91	116.4	2.5	927	5	AAI65877	Aai65877 Nucleotid
92	114.8	2.4	575	13	ACN58193	Acn58193 Cotton gy

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 17:55:53 ; Search time 17929.4 Seconds
(without alignments)
12264.715 Million cell updates/sec

Title: US-08-939-905D-2
Perfect score: 4700
Sequence: 1 tagataaaaaaaatgggat.....ttaagggtacttaattaatca 4700

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_hlc:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_gse1:
10: gb_gse2:
11: gb_gse3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	667	14.2	766	2	BE659320
C 2	625	13.3	664	2	BE822567
C 3	582	12.4	663	2	BE822838
C 4	492	10.5	494	1	AW277864
C 5	490	10.4	540	2	BE660610
C 6	480	10.2	518	1	AW704748
C 7	479.4	10.2	546	1	AW278026
C 8	479	10.2	541	1	AW279469
C 9	471.2	10.0	803	2	BE660615
C 10	465.6	9.9	583	1	AI960823
C 11	427	9.1	427	2	BE610364
C 12	422.4	9.0	592	1	AW704659
C 13	413.2	8.8	602	1	AW705617
C 14	387	8.2	584	1	AW705730
C 15	384.2	8.2	639	2	BE608629
C 16	378.2	8.0	448	2	BE653639
C 17	361.4	7.7	363	1	AW706826
C 18	327	7.0	370	1	AW704798
C 19	323	6.9	333	1	AW596852
C 20	314	6.7	342	1	AW705740
C 21	306	6.5	691	1	AW278775
C 22	304.8	6.5	632	6	CA919442

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 17:55:53 ; Search time 4745.58 Seconds
(without alignments)
12264.715 Million cell updates/sec

Title: US-08-939-905D-1
Perfect score: 1244
Sequence: 1 atgggttcacatggtctatt.....ttaaggctacttaataatca 1244

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hlc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	780	62.7	824	1	AI959837
2	731	58.8	766	2	BE659320
3	678	54.5	691	2	BE660616
4	665	53.5	691	1	AW278775
5	649.2	52.2	672	1	AW185769
6	639	51.4	663	2	BE822838
7	625.4	50.3	648	2	BE660617
8	625	50.2	664	2	BE822567
9	623	50.1	639	2	BE608629
10	598	48.1	610	2	BE660609
11	589.2	47.4	803	2	BE660615
12	585	47.0	597	2	BE660608
13	583	46.9	584	1	AW705730
14	582.6	46.8	850	6	CB893969
15	582.2	46.8	606	1	AI960938
16	581.4	46.7	592	1	AW704659
17	579.4	46.6	602	1	AW705617
18	579.2	46.6	608	1	AW705946
19	567.6	45.6	583	1	AI960823
20	559.8	45.0	566	1	AW705638
21	544.4	43.8	546	1	AW278026
22	539	43.3	541	1	AW279469